OM nucleic - nucleic search, using sw model

Run on:　　　February 18, 2004, 15:41:57 ; Search time 0.001 Seconds
　　　　　　　　　　　　　　　　　　　　(without alignments)
　　　　　　　　　　　　　　　　　　　　1.000 Million cell updates/sec

Title:
Perfect score:　　20
Sequence:　　　　1 gaaaccaaggcacagtggaa 20
Title:　　　　　　us-09-960-143-58

Scoring table:　　IDENTITY.NUC
　　　　　　　　　　Gapop 10.0 , Gapext 0.5

Searched:　　　　1 seqs, 25 residues

Total number of hits satisfying chosen parameters:　　2

Minimum DB seq length: 20
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
　　　　　　　　　　Maximum Match 100%
　　　　　　　　　　Listing first 1 summaries

Database :　　　rnpb.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	DB ID	Description
1	20	100.0	25	1	US-09-885-441-31	Sequence 31, Appl

ALIGNMENTS

RESULT 1
US-09-885-441-31
; Sequence 31, Application US/09885441
; Patent No. US20020146407A1
; GENERAL INFORMATION:
; APPLICANT: Xiao, Yonghong
; TITLE OF INVENTION: Regulation of Human Eosinophil Serine
; TITLE OF INVENTION: Protease-1-Like Enzyme
; FILE REFERENCE: 04974.00512
; CURRENT APPLICATION NUMBER: US/09/885,441
; CURRENT FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/212,844

Query Match　　　100.0%;　Score 20;　DB 1;　Length 25;
Best Local Similarity　100.0%;　Pred. No. 0;
Matches　20;　Conservative　0;　Mismatches　0;　Indels　0;　Gaps　0;

Qy　　1 GAAACCAAGGCACAGTGGAA 20
　　　　||||||||||||||||||||
Db　　4 GAAACCAAGGCACAGTGGAA 23

Search completed: February 18, 2004, 15:41:58
Job time : 1 secs

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Run on:          February 18, 2004, 15:43:34 ; Search time 0.001 seconds
                                              (without alignments)
                                              5.200 Million cell updates/sec

Title:           us-09-960-143-58
Perfect score:   20
Sequence:        1 gaaaccaaggcacagtggaa 20

Scoring table:   IDENTITY.NUC
                 Gapop 10.0 , Gapext 0.5

Searched:        6 seqs, 130 residues

Database :       rnpm.seq:*

Total number of hits satisfying chosen parameters:     12

Minimum DB seq length: 20
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 6 summaries

            Pred. No. is the number of results predicted by chance to have a
            score greater than or equal to the score of the result being printed,
            and is derived by analysis of the total score distribution.

                                SUMMARIES

Result        %
No.   Score Query Match Length DB  ID                   Description
-------------------------------------------------------------------
1     20    100.0       20    1   PCT-US02-29992-58    Sequence 58, Appl
2     20    100.0       20    1   US-09-960-143-58     Sequence 58, Appl
3     20    100.0       25    1   US-09-885-441-31     Sequence 31, Appl
4     20    100.0       25    1   US-10-424-836-31     Sequence 31, Appl
5     14    70.0        20    1   PCT-US02-29992-57    Sequence 57, Appl
6     14    70.0        20    1   US-09-960-143-57     Sequence 57, Appl

                                ALIGNMENTS

RESULT 1
PCT-US02-29992-58
; Sequence 58, Application PC/TUS0229992
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Brenda F. Baker
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 8 EXPRESSION
; FILE REFERENCE: RTSP-0417
; CURRENT APPLICATION NUMBER: PCT/US02/29992
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 09/960,143
;

Query Match          100.0%;   Score 20;   DB 1;   Length 20;
Best Local Similarity   100.0%;
Matches   20;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy   1 GAAACCAAGGCACAGTGGAA 20
       ||||||||||||||||||||
Db   1 GAAACCAAGGCACAGTGGAA 20


RESULT 2
US-09-960-143-58
; Sequence 58, Application US/09960143
; GENERAL INFORMATION:
; APPLICANT: Brenda F. Baker
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 8 EXPRESSION
; FILE REFERENCE: RTS-0266
; CURRENT APPLICATION NUMBER: US/09/960,143
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 58

Query Match          100.0%;   Score 20;   DB 1;   Length 20;
Best Local Similarity   100.0%;
Matches   20;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy   1 GAAACCAAGGCACAGTGGAA 20
       ||||||||||||||||||||
Db   1 GAAACCAAGGCACAGTGGAA 20


RESULT 3
US-09-885-441-31
; Sequence 31, Application US/09885441
; GENERAL INFORMATION:
; APPLICANT: Xiao, Yonghong
; TITLE OF INVENTION: Regulation of Human Eosinophil Serine
; TITLE OF INVENTION: Protease-1-Like Enzyme
; FILE REFERENCE: 04974.00512
; CURRENT APPLICATION NUMBER: US/09/885,441
; CURRENT FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/212,844
; PRIOR FILING DATE: 2000-06-21
;

Query Match          100.0%;   Score 20;   DB 1;   Length 25;
Best Local Similarity   100.0%;
Matches   20;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy   1 GAAACCAAGGCACAGTGGAA 20
       ||||||||||||||||||||
Db   4 GAAACCAAGGCACAGTGGAA 23


RESULT 4
US-10-424-836-31
; Sequence 31, Application US/10424836
; GENERAL INFORMATION:
; APPLICANT: Xiao, Yonghong
; TITLE OF INVENTION: Regulation of Human Eosinophil Serine
; TITLE OF INVENTION: Protease-1-Like Enzyme
; FILE REFERENCE: 04974.00512
; CURRENT APPLICATION NUMBER: US/10/424,836
; CURRENT FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: US/09/885,441
; PRIOR FILING DATE: 2001-06-21
;

Query Match          100.0%;   Score 20;   DB 1;   Length 25;
Best Local Similarity   100.0%;
Matches   20;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy   1 GAAACCAAGGCACAGTGGAA 20
       ||||||||||||||||||||
Db   4 GAAACCAAGGCACAGTGGAA 23


RESULT 5
PCT-US02-29992-57
; Sequence 57, Application PC/TUS0229992
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Brenda F. Baker
; APPLICANT: Susan M. Freier
```

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Run on:         February 18, 2004, 15:44:47 ; Search time 0.001 Seconds
                                              (without alignments)
                                              1.000 Million cell updates/sec

Title:          us-09-960-143-58
Perfect score:  20
Sequence:       1 gaaaccaaggcacagtggaa 20

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 0.5

Searched:       1 seqs, 25 residues

Total number of hits satisfying chosen parameters:      2

Minimum DB seq length: 20
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 1 summaries

Database :      rnpn.seq:*

                Pred. No. is the number of results predicted by chance to have a
                score greater than or equal to the score of the result being printed,
                and is derived by analysis of the total score distribution.

                                    SUMMARIES

Result               Query                      %
No.     Score    Match Length DB  ID                  Description
------  -----    ----- ------ --  --                  -----------
c   1    20      100.0   25    1  US-09-953-115A-13471 Sequence 13471, A
```

                                    ALIGNMENTS

```
RESULT 1
US-09-953-115A-13471/c
Sequence 13471, Application US/09953115A
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Analysis of Human Genes
; FILE REFERENCE: 3111.1
; CURRENT APPLICATION NUMBER: US/09/953,115A
; CURRENT FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: 60/232,597
; PRIOR FILING DATE: 2000-09-14
; NUMBER OF SEQ ID NOS: 33029

Query Match           100.0%;  Score 20;  DB 1;  Length 25;
Best Local Similarity 100.0%;
Matches  20;  Conservative   0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy         1 GAAACCAAGGCACAGTGGAA 20
             ||||||||||||||||||||
Db        25 GAAACCAAGGCACAGTGGAA 6
```

Search completed: February 18, 2004, 15:44:47
Job time : 0.001 secs